

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,522  
Source: IFWP  
Date Processed by STIC: 4/10/06

# ***ENTERED***

IFWP

## RAW SEQUENCE LISTING

DATE: 04/10/2006

PATENT APPLICATION: US/10/573,522

TIME: 10:43:31

Input Set : A:\082368-007400US.txt

Output Set: N:\CRF4\04102006\J573522.raw

```

4 <110> APPLICANT: Nakamura, Yusuke
5     Katagiri, Toyomasa
6     Nakatsuru, Shuichi
8 <120> TITLE OF INVENTION: METHOD OF DIAGNOSING BREAST CANCER
11 <130> FILE REFERENCE: 082368-007400US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/573,522
C--> 13 <141> CURRENT FILING DATE: 2006-03-23
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/011741
14 <151> PRIOR FILING DATE: 2004-08-10
16 <150> PRIOR APPLICATION NUMBER: US 60/505,571
17 <151> PRIOR FILING DATE: 2003-09-24
19 <160> NUMBER OF SEQ ID NOS: 34
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 928
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (127)...(720)
32 <400> SEQUENCE: 1
33 ggcgcgcagcg ctggtacccc gttggtccgc gcgttgctgc gttgtgaggg gtgtcagctc 60
34 agtgcacccc aggcagctct tagtgtggag cagtgaactg tgtgtgggtc cttctacttg 120
35 gggatc atg cag aga gct tca cgt ctg aag aga gag ctg cac atg tta 168
36     Met Gln Arg Ala Ser Arg Leu Lys Arg Glu Leu His Met Leu
37         1             5             10
39 gcc aca gag cca ccc cca ggc atc aca tgt tgg caa gat aaa gac caa 216
40 Ala Thr Glu Pro Pro Pro Gly Ile Thr Cys Trp Gln Asp Lys Asp Gln
41 15             20             25             30
43 atg gat gac ctg cga gct caa ata tta ggt gga gcc aac aca cct tat 264
44 Met Asp Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr
45             35             40             45
47 gag aaa ggt gtt ttt aag cta gaa gtt atc att cct gag agg tac cca 312
48 Glu Lys Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro
49             50             55             60
51 ttt gaa cct cct cag atc cga ttt ctc act cca att tat cat cca aac 360
52 Phe Glu Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn
53             65             70             75
55 att gat tct gct gga agg att tgt ctg gat gtt ctc aaa ttg cca cca 408
56 Ile Asp Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro
57             80             85             90
59 aaa ggt gct tgg aga cca tcc ctc aac atc gca act gtg ttg acc tct 456
60 Lys Gly Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser

```

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```

61 95          100          105          110
63 att cag ctg ctc atg tca gaa ccc aac cct gat gac ccg ctc atg gct 504
64 Ile Gln Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala
65          115          120          125
67 gac ata tcc tca gaa ttt aaa tat aat aag cca gcc ttc ctc aag aat 552
68 Asp Ile Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn
69          130          135          140
71 gcc aga cag tgg aca gag aag cat gca aga cag aaa caa aag gct gat 600
72 Ala Arg Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp
73          145          150          155
75 gag gaa gag atg ctt gat aat cta cca gag gct ggt gac tcc aga gta 648
76 Glu Glu Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val
77          160          165          170
79 cac aac tca aca cag aaa agg aag gcc agt cag cta gta ggc ata gaa 696
80 His Asn Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu
81 175          180          185          190
83 aag aaa ttt cat cct gat gtt tag gggacttgct ctgggttcac ttagttaatg 750
84 Lys Lys Phe His Pro Asp Val *
85          195
87 tggttctttgc caaggtgatc taagttgcct accttgaatt tttttttaaa tatatttgat 810
88 gacataattt ttgtgtagtt tatttatctt gtacatatgt attttgaaat cttttaaac 870
89 tgaaaaataa atagtcattt aatgttgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 928
91 <210> SEQ ID NO: 2
92 <211> LENGTH: 197
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 2
97 Met Gln Arg Ala Ser Arg Leu Lys Arg Glu Leu His Met Leu Ala Thr
98 1          5          10          15
99 Glu Pro Pro Pro Gly Ile Thr Cys Trp Gln Asp Lys Asp Gln Met Asp
100          20          25          30
101 Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr Glu Lys
102          35          40          45
103 Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro Phe Glu
104          50          55          60
105 Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn Ile Asp
106 65          70          75          80
107 Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro Lys Gly
108          85          90          95
109 Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser Ile Gln
110          100          105          110
111 Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala Asp Ile
112          115          120          125
113 Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn Ala Arg
114          130          135          140
115 Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp Glu Glu
116 145          150          155          160
117 Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val His Asn
118          165          170          175

```

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```

119 Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu Lys Lys
120                180                185                190
121 Phe His Pro Asp Val
122                195
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 1472
127 <212> TYPE: DNA
128 <213> ORGANISM: Homo sapiens
130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (53)...(1189)
134 <400> SEQUENCE: 3
135 ggccactgag ccggggtgca gtggcagcgg gagagtacct ggcgatggcg at atg agc 58
136                                     Met Ser
137                                     1
139 ggt gcg ggg gtg gcg gct ggg acg cgg ccc ccc agc tcg ccg acc ccg 106
140 Gly Ala Gly Val Ala Ala Gly Thr Arg Pro Pro Ser Ser Pro Thr Pro
141                5                10                15
143 ggc tct cgg cgc cgg cgc cag cgc ccc tct gtg ggc gtc cag tcc ttg 154
144 Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln Ser Leu
145                20                25                30
147 agg ccg cag agc ccg cag ctc agg cag agc gac ccg cag aaa cgg aac 202
148 Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys Arg Asn
149 35                40                45                50
151 ctg gac ctg gag aaa agc ctg cag ttc ctg cag cag cag cac tcg gag 250
152 Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His Ser Glu
153                55                60                65
155 atg ctg gcc aag ctc cat gag gag atc gag cat ctg aag cgg gaa aac 298
156 Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg Glu Asn
157                70                75                80
159 aag gat ctc cat tac aag ctc ata atg aat cag aca tca cag aag aaa 346
160 Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln Lys Lys
161                85                90                95
163 gat ggc ccc tca gga aac cac ctt tcc agg gcc tct gct ccc ttg ggc 394
164 Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro Leu Gly
165                100                105                110
167 gct cgc tgg gtc tgc atc aac gga gtg tgg gta gag ccg gga gga ccc 442
168 Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly Gly Pro
169 115                120                125                130
171 agc cct gcc agg ctg aag gag ggc tcc tca cgg aca cac agg cca gga 490
172 Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg Pro Gly
173                135                140                145
175 ggc aag cgt ggg cgt ctt gcg ggc ggt agc gcc gac act gtg cgc tct 538
176 Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val Arg Ser
177                150                155                160
179 cct gca gac agc ctc tcc atg tca agc ttc cag tct gtc aag tcc atc 586
180 Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys Ser Ile
181                165                170                175
183 tct aat tca ggc aag gcc agg ccc cag ccc ggc tcc ttc aac aag caa 634

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```

184 Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn Lys Gln
185      180      185      190
187 gat tca aaa gct gac gtc tcc cag aag gcg gac ctg gaa gag gag ccc 682
188 Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu Glu Pro
189 195      200      205      210
191 cta ctt cac aac agc aag ctg gac aaa gtt cct ggg gta caa ggg cag 730
192 Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln Gly Gln
193      215      220      225
195 gcc aga aag gag aaa gca gag gcc tct aat gca gga gct gcc tgt atg 778
196 Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala Cys Met
197      230      235      240
199 ggg aac agc cag cac cag ggc agg cag atg ggg gcg ggg gca cac ccc 826
200 Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala His Pro
201      245      250      255
203 cca atg atc ctg ccc ctt ccc ctg cga aag ccc acc aca ctt agg cag 874
204 Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu Arg Gln
205      260      265      270
207 tgc gaa gtg ctc atc cgc gag ctg tgg aat acc aac ctc ctg cag acc 922
208 Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu Gln Thr
209 275      280      285      290
211 caa gag ctg cgg cac ctc aag tcc ctc ctg gaa ggg agc cag agg ccc 970
212 Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln Arg Pro
213      295      300      305
215 cag gca gcc ccg gag gaa gct agc ttt ccc agg gac caa gaa gcc acg 1018
216 Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu Ala Thr
217      310      315      320
219 cat ttc ccc aag gtc tcc acc aag agc ctc tcc aag aaa tgc ctg agc 1066
220 His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys Leu Ser
221      325      330      335
223 cca cct gtg gcg gag cgt gcc atc ctg ccc gca ctg aag cag acc ccg 1114
224 Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln Thr Pro
225      340      345      350
227 aag aac aac ttt gcc gag agg cag aag agg ctg cag gca atg cag aaa 1162
228 Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met Gln Lys
229 355      360      365      370
231 cgg cgc ctg cat cgc tca gtg ctt tga gccaccccaa tctggtcagt 1209
232 Arg Arg Leu His Arg Ser Val Leu *
233      375
235 gccaggccca ccaacctgca gctggagact ggctctctat agcatttcct gatacttccg 1269
236 ctactttttag gcttggtctaa attccaagac agataacact caagatagat aaagtacttg 1329
237 atctccaaac tgacaaactg tttatatttct agctgttatt ttgctatttg gcatttacat 1389
238 aaaagcacac gatgaagcag gtatcgctt acctgttgaa actgaaaata aagcttggtt 1449
239 atttccaaaa aaaaaaaaaa aaa 1472
241 <210> SEQ ID NO: 4
242 <211> LENGTH: 378
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 4
247 Met Ser Gly Ala Gly Val Ala Ala Gly Thr Arg Pro Pro Ser Ser Pro

```

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```

248 1          5          10          15
249 Thr Pro Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln
250          20          25          30
251 Ser Leu Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys
252          35          40          45
253 Arg Asn Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His
254          50          55          60
255 Ser Glu Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg
256 65          70          75          80
257 Glu Asn Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln
258          85          90          95
259 Lys Lys Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro
260          100         105         110
261 Leu Gly Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly
262          115         120         125
263 Gly Pro Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg
264          130         135         140
265 Pro Gly Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val
266 145         150         155         160
267 Arg Ser Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys
268          165         170         175
269 Ser Ile Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn
270          180         185         190
271 Lys Gln Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu
272          195         200         205
273 Glu Pro Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln
274          210         215         220
275 Gly Gln Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala
276 225         230         235         240
277 Cys Met Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala
278          245         250         255
279 His Pro Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu
280          260         265         270
281 Arg Gln Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu
282          275         280         285
283 Gln Thr Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln
284          290         295         300
285 Arg Pro Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu
286 305         310         315         320
287 Ala Thr His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys
288          325         330         335
289 Leu Ser Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln
290          340         345         350
291 Thr Pro Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met
292          355         360         365
293 Gln Lys Arg Arg Leu His Arg Ser Val Leu
294          370         375
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 1315

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/573,522

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Input Set : A:\082368-007400US.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date